IN THE CLAIMS:

This is a complete listing of the claims as they stand following the Article 19 Amendments.

1. (Previously presented) Seed of cotton event designated MON 88913 comprising SEQ ID NO:1 and SEQ ID NO:2 and having representative seed deposited with American Type Culture Collection (ATCC) with Accession No. PTA-4854.

2. (Original) The cotton plant or parts thereof produced by growing the seed of claim 1.

3. (Original) The cotton plant or parts thereof of claim 2, comprising pollen, ovule, flowers, boils, lint, shoots, roots, or leaves.

4. (Original) Glyphosate tolerant progeny of the cotton plant of claim 2.

5. (Original) A progeny cotton plant of claim 4, wherein the genome of said cotton plant comprises one or more DNA molecules selected from the group consisting of SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO:3, and SEQ ID NO:4.

6. (Previously presented) A progeny cotton plant or seed or parts thereof of claim 4, the genome of which produces an amplicon comprising SEQ ID NO: 1 or SEQ ID NO:2 in a DNA amplification method.

7. (Previously presented) A DNA primer set comprising two DNA molecules, wherein the first DNA molecule comprises at least 11 or more contiguous polynucleotides of any portion of the transgene region of the DNA molecule of SEQ ID NO:3 or its complement, and the second DNA molecule of similar length comprises any portion of a 5' flanking cotton genomic DNA region of SEQ ID NO:3 or its complement, where these DNA molecules when used together are useful in a DNA amplification method to produce an amplicon comprising SEQ ID NO: 1 diagnostic for cotton event MON 88913.

8. (Previously presented) A DNA primer set comprising two DNA molecules, wherein the first DNA molecule comprises at least 11 or more contiguous polynucleotides of any portion of the

transgene region of the DNA molecule of SEQ ID NO:4, or its complement, and the second DNA molecule of similar length comprises any portion of a 3' flanking cotton genomic DNA region of SEQ ID NO:4, or its complement, where these DNA molecules when used together are useful as a DNA primer set in a DNA amplification method to produce an amplicon comprising SEQ ID NO:2 diagnostic for cotton event MON 88913.

9. (Original) A DNA detection kit comprising at least one molecule of 11 or more contiguousnucleotides homologous or complementary to SEQ ID NO:3 or SEQ ID NO:4, that when used in a DNA amplification methods produces an amplicon comprising SEQ ID NO: 1 or SEQ ID NO:2 diagnostic for cotton event MON 88913.

10. (Previously presented) A method of producing a cotton plant that tolerates application of glyphosate herbicide comprising:

(a) sexually crossing a first glyphosate tolerant cotton event MON 88913 parent plant comprising SEQ ID NO:1 and SEQ ID NO:2 and a second parent cotton plant that lacks the tolerance to glyphosate herbicide, thereby producing a plurality of first progeny plants; and

(b) selecting a first progeny plant that is tolerant to glyphosate; and

(c) selfing said first progeny plant, thereby producing a plurality of second progeny plants; and

(d) selecting from said second progeny plants, a glyphosate tolerant plant.

11. (Original) The method of claim 10 further comprising the step of backcrossing the first progeny plant that is tolerant to glyphosate or the second progeny plant that is glyphosate tolerant to the second parent plant or a third parent plant, thereby producing a plant that tolerates the application of glyphosate.

12. (Previously presented) A method of detecting the presence of DNA corresponding to cotton event MON 88913 comprising SEQ ID NO:1 and SEQ ID NO:2 in a sample, the method comprising:

(a) contacting the sample comprising DNA with a DNA primer set comprising

(i) at least 11 contiguous nucleotides of a 5' flanking cotton genomic DNA region flanking the insertion site in cotton event MON88913 or its complement, or a 3'

flanking cotton genomic DNA region flanking the insertion site in cotton event MON88913 or its complement, and

(ii) at least 11 contiguous nucleotides of the transgene region of SEQ ID NO:3 or SEQ ID NO:4; which when used in a nucleic acid amplification reaction with genomic DNA from the cotton event MON 88913, produces a diagnostic amplicon comprising SEQ ID NO:1 or SEQ ID NO:2;and

(b) performing a nucleic acid amplification reaction, thereby producing a sample amplicon; and

(c) comparing the sample amplicon to the diagnostic amplicon to determine whether the sample amplicon comprises SEQ ID NO:1 or SEQ ID NO:2.

13. (Original) In the method of claim 12, where in said primer set comprises SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:24.

14. (Original) In the method of claim 12, wherein said primer set comprises SEQ ID NO:26, SEQ ID NO:27 and SEQ ID NO:28.

15. (Previously presented) A method of detecting the presence of a DNA corresponding to cotton event MON 88913 in a sample, the method comprising:

(a) contacting the sample comprising DNA with a probe that hybridizes under stringent hybridization conditions with genomic DNA from the cotton event MON 88913, comprising SEQ ID NO:1 and SEQ ID NO:2, and does not hybridize under the stringent hybridization conditions with a control cotton plant genomic DNA, wherein said probe is homologous or complementary to SEQ ID NO:1 or SEQ ID NO:2; and

(b) subjecting the sample and probe to stringent hybridization conditions; and

(c) detecting hybridization of the probe to the DNA.

16. (Original) A cotton plant comprising a glyphosate tolerant trait that is genetically linked to a complement of a marker polynucleic acid, wherein said marker polynucleic acid molecule is homologous or complementary to a DNA molecule selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:2.

17. (Original) A method of determining the zygosity of the progeny of cotton event MON 88913 comprising:

(a) contacting the sample comprising cotton DNA with a primer set comprising SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:23, that when used in a nucleic-acid amplification reaction with genomic DNA from cotton event MON 88913, produces a first amplicon that is diagnostic for cotton event MON 88913; and

(b) performing a nucleic acid amplification reaction, thereby producing the first amplicon; and

(c) detecting the first amplicon; and

(d) contacting the sample comprising cotton DNA with said primer set, that when used in a nucleic-acid amplification reaction with genomic DNA from cotton plants produces a second amplicon comprising the native cotton genomic DNA homologous to the cotton genomic region of a transgene insertion identified as cotton event MON 88913;

(e) performing a nucleic acid amplification reaction, thereby producing the second amplicon; and

(f) detecting the second amplicon; and

(g) comparing the first and second amplicons in a sample, wherein the presence of both amplicons indicates the sample is heterozygous for the transgene insertion.

18. (Original) A method of determining the zygosity of the progeny of cotton event MON 88913 comprising:

(a) contacting the sample comprising cotton DNA with a primer set comprising SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, and SEQ ID NO:25: and

(b) performing a nucleic acid amplification reaction; and

(c) detecting the products of the reaction.

19. (Previously presented) A method for controlling weeds in a crop of cotton event MON 88913, comprising SEQ ID NO:1 and SEQ ID NO:2, comprising the step of applying an effective dose of a glyphosate containing herbicide to said crop of cotton event MON 88913.

20. (Previously presented) The method of claim 12, wherein the DNA primer set comprises at least one molecule of 11 or more contiguous nucleotides homologous or complementary to SEQ ID NO:3 or SEQ ID NO:4.